DNA-Based, Marker-Assisted Selection in Beef Cattle

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Genetic improvement through selection has been one of the most important contributors to the advancements in animal productivity in the past 50 years. Traditionally, selection in beef cattle has been based on estimating breeding value using expected progeny difference (EPDs). The EPDs are derived from the observable performance (or phenotype) of the animal and its relatives. EPDs statistically predict that animal's genetic potential for given traits (e.g., weaning weight). The accuracy of the estimate will increase over time as more information from progeny and relatives becomes available.

EPDs are the tools. They are not the plan. In order to effectively use EPDs, it is important to develop a breeding plan with specific goals and objectives (e.g., the most profitable selection criteria) for your herd or production system. Most of the economically relevant traits for cattle production (birth weight, weaning weight, growth, reproduction, milk production, carcass quality, etc.) are complex traits controlled by many genes and influenced by the production environment.

A gene is a segment of deoxyribonucleic acid (DNA) that is made up of pairs of four nucleotides abbreviated as "A", "C", "G", and "T" (see Fig. 1 on the next page). A gene dictates the production of a specific protein. It is possible for the sequence of the DNA that makes up a gene to differ between individuals. These DNA variations in a gene are called alleles, and they often result in differences in the amount or type of protein being produced by that gene among different individual animals.

The protein produced by different alleles may affect the expression of a given trait and influence the observed performance. When an animal has an EPD above the base year average for a certain trait, what that means is that the animal inherited a higher than average proportion of alleles that favorably affect the trait.

It should be noted that traditional selection methods inherently tend to increase the frequency of alleles that have major beneficial effects on selected traits. That is, EPDs as typically used, increase the number of favorable alleles without knowing which specific genes are involved. This contrasts with DNA-based selection where knowledge of which DNA sequences are associated with improvement in a given trait is required, and selection is focused on those known DNA "markers" to make genetic improvement in the trait.

Recently scientists have started to identify regions of DNA that influence production traits. They have used molecular techniques to find differences in the sequence of the nucleotide base pairs in these regions. Tests have been developed to identify these subtle differences in the DNA. This has allowed for the development of genetic markers that scientists can use to identify whether an animal is carrying a segment of DNA that is positively or negatively associated with the trait of interest.

Genetic markers in a given region of DNA may differ from each other by the sequence of only a single nucleotide base pair, such as a single A, C, G, or T (Fig. 1). Such differences are called single nucleotide polymorphisms or SNPs (referred to as "snips"). Genetic tests based on SNPs analyze DNA derived from an individual to determine the DNA sequence that is present at one specific location (nucleotide pair) in among the three billion nucleotide pairs that comprise the genome of the cow!

Genotyping is the term that is used to describe the process of using laboratory methods to determine the sequence of nucleotides in the DNA from an individual, usually at one particular gene or specific location in the genome.

Selecting an animal carrying the favorable form of a marker, or one that is associated with a positive impact
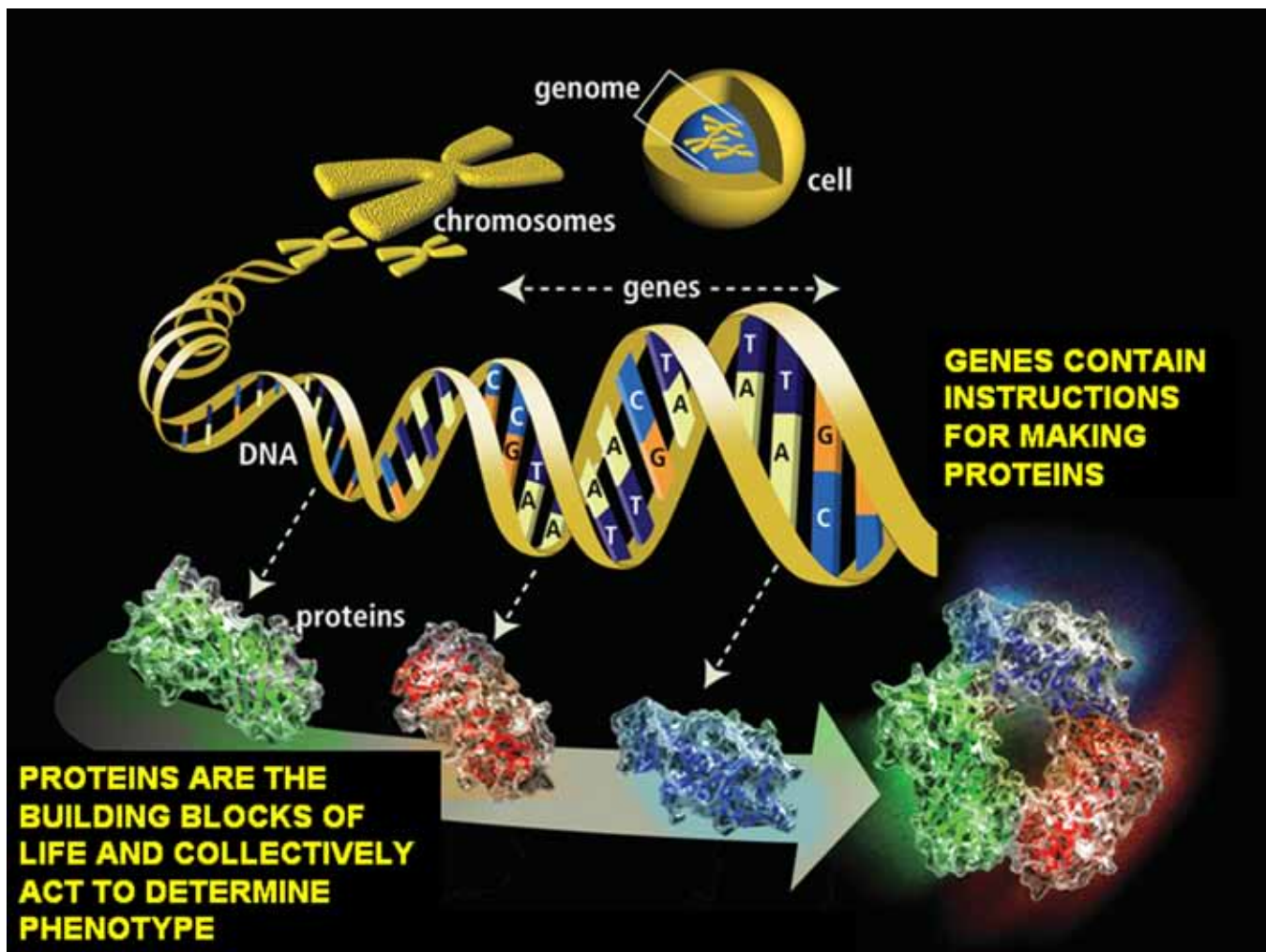
Fig. 1. DNA (deoxyribonucleic acid) contains the instructions for making proteins. Differences in the nucleotide sequence of a gene's DNA can influence the type or amount of protein that is made, and this can have an effect on the observed performance of an animal. Source: Original graphic obtained with permission from the U.S. Department of Energy Human Genome Program (http://www.doegenomes.org).

on the trait of interest, can result in an improvement in the observed phenotype for that trait. Although complex traits are influenced by several genes, the mode of inheritance of each genetic marker is simple. An animal gets one marker allele from both its sire and dam.

Marker-Assisted Selection (MAS) is the process of using the results of DNA tests to assist in the selection of individuals to become the parents in the next generation of a genetic improvement program**.** Genotyping allows for the accurate detection of specific DNA variations that have been associated with measurable effects on complex traits. It is important to remember that markers for complex traits are associated with only one of the many genes that contribute toward that trait.

The presence or absence of the numerous other "unmarked" genes and the production environment will determine whether an animal actually displays the desired phenotype (e.g., large weaning weight, increased marbling). EPDs estimate the breeding value of all the genes (both "marked" and "unmarked") that contribute

toward a given trait and, therefore, should always be considered in selection decisions, even when marker data are available.

Potential benefits from marker-assisted selection are greatest for traits that:

1. Have low heritability (e.g., traits where observed or measured values are poor predictors of breeding value) (Table 1).
2. Are difficult or expensive to measure (e.g., disease resistance).
3. Cannot be measured until after the animal has already contributed to the next generation (e.g., carcass data).
4. Are currently not selected for as they are not routinely measured (e.g., tenderness).
5. Are phenotypically (observed value), but not genetically, correlated with a trait that you do not want to increase (e.g., selection for marbling markers does not genetically increase backfat thickness despite the fact that on the animal these two traits tend to increase in unison).

Table 1. Heritability estimates for important beef cattle traits. (Source: Taylor and Field 2002)

Trait(s)	Heritability[a] (%)
Reproductive	
Age at puberty	40
Weight at puberty	50
Scrotal circumference	50
Breeding soundness examination	10
Primary sperm abnormalities	30
Secondary sperm abnormalities	2
Reproductive tract score	30
First service conception rate	25
Calving date	20
Calving ease	15
Weight at puberty	40
Gestation length	40
Birth weight	40
Pelvic area	50
Body condition score	40
Calving interval	10
Multiple births	5
Growth	
Weaning weight	30
Milk production	20
Postweaning ADG (feedlot)	45
Postweaning ADG (pasture)	30
Efficiency of feedlot gain	45
Maintenance (MEm)	50
Yearling weight	40
Mature weight	50
Carcass	
Carcass weight (at similar age)	40
Carcass quality grade	35
Fat thickness	45
Yearling hip height	40
Yield grade	35
Tenderness	25
Shear force (WBS)	40
Sensory panel	10

[a]Heritabilities below 20 percent are considered low, those 20 to 39 percent are considered medium, and those 40 percent and higher reflect highly heritable traits.

In order of greatest to least degree of benefit, the following categories of traits are likely to benefit the most from marker-assisted selection: (1) disease resistance, (2) carcass quality and palatability attributes, (3) fertility and reproductive efficiency, (4) carcass quantity and yield, and (5) milk production, maternal ability, and growth performance.

This ranking is due to a combination of considerations including: (1) relative difficulty in collecting performance data, (2) relative magnitude of the heritability and phenotypic variation observed in the traits, (3) current amount of performance information available, and (4) when performance data become available in the life cycle.

Recently genetic tests for DNA markers associated with marbling and tenderness have become commercially available. Each of these markers is associated with only one of the genes that contribute toward marbling or tenderness. Other "unmarked" genes, in conjunction with the production setting, will influence whether an animal marbles or has tender meat. Cattle can be genotyped for the desirable form of the marker by analyzing DNA collected from hair, tissue, blood, or semen samples.

It is important to have some idea of how much of the variability for a given trait is accounted for by each DNA marker. Ideally, but not necessarily, the preferred form of a marker would always identify genetically superior animals. Results from studies in commercial herds, comparing the performance of animals with and without the marker, should be an important consideration as they can help to estimate the effect of the marker on the trait under commercial conditions.

In the future it is likely that phenotypic, pedigree, and DNA-marker information will all be included in EPD calculations and that selection on this EPD will be superior to selection based on markers alone. The challenge will be to ensure that the value derived from the genetic progress associated with marker assisted selection for marbling and tenderness, or any other trait, outweighs the expense of collecting the marker information.

How Much Weight Should Be Given to Market-Assisted Selection vs. EPDs?

This is really the most important question for producers, and one that is not easily answered as it will differ for every producer based upon the production system, genotyping costs, and marketing considerations. The following questions should be asked when evaluating the use of marker-assisted selection in a breeding program.

Will marker-assisted selection make you money? For marker-assisted selection to be profitable, the increased economic returns from greater genetic gain as a result of using the markers must outweigh the cost of genotyping. Producers need to consider how they are being financially compensated for achieving an improved rate of genetic improvement in the trait that is associated with a given genetic marker.

How much of the genetic variation in the trait of interest does this marker explain in your herd? Ideally markers should account for a large proportion of the variability in a trait. In other words, the marker should have a big effect on the trait of interest. The genetic gain that can be achieved by using marker-assisted selection depends on the amount of genetic variation that is accounted for by the marker. If the marker only accounts for a small amount of the genetic variability for a trait, then little genetic improvement will be made by simply focusing on increasing the frequency of the marker. Likewise, if all of the animals in a given herd carry two copies, or no copies, of a given marker, then

no genetic progress can be achieved by using marker-assisted selection since the marker accounts for none of the genetic variability seen for the trait in that herd.

What are you giving up to use animals that are carrying the marker of interest? Selection usually focuses on more than one trait. It is important not to narrow down the set of animals eligible for selection based solely on their genotype for a marker associated with only one trait. Selecting from a smaller set of animals that carry the marker could eliminate animals with high EPDs for other economically relevant traits. This will decrease the intensity of selection, and hence genetic progress, which is being made for these other traits. Also, special care should be taken to ensure that selection for the marker does not negatively affect genetic improvement in other traits of economic importance.

Could good progress in that trait be achieved without the expense of marker-assisted selection, such as using EPDs? Markers are most useful for traits that are not routinely recorded (have no phenotypic measurement), and traits that have low accuracy EPDs. Also, as trait heritability increases, the improvement in selection response as a result of using marker information is reduced relative to selection based on EPDs alone.

Once a decision has been made to use marker-assisted selection, the actual application of the technology is fairly straightforward. Blood, hair (including the roots), or semen samples should be collected from potential sires and dams and sent for testing to determine the genotype of each animal for the specific marker of interest. To increase the frequency of a marker that is positively associated with the trait of interest, producers need to select for animals that are carrying two copies of the marker, and against those carrying no copies of the marker.

All of the offspring from a parent carrying two copies of the marker (homozygous) will inherit a copy of the marker from that parent. In a typical herd, selection for homozygous sires will probably be the most rapid way to increase the frequency of the marker. Marker-assisted pre-selection of sires for progeny testing may also be useful to rapidly increase the proportion of sires that carry the genetic marker and pass it on to their progeny. Continuous use of homozygous sires for four generations will result in about 90 percent of the herd carrying two copies of the marker.

> **Marker-assisted selection should be viewed as a tool to assist with, and not as a replacement for, traditional selection techniques.**

Web Sites for U.S. Companies Providing Genotyping Services for Beef Cattle

- http://www.bovigensolutions.com
  Parentage, GeneSTAR marbling, GeneSTAR tenderness 2

- http://www.geneticvisions.net
  Coat color, Prolactin *(CMP),* BLAD, Citrullinemia, DUMPS, Kappa-Casein, Beta-lactoglobulin, Complex Vertebral Malformation

- http://www.genmarkag.com
  Parentage, coat color, BLAD, Citrullinemia, MSUD, Kappa-Casein, Beta-lactoglobulin, AlphaS1-casein, Piedmontese Myostatin

- http://www.igenity.com
  Parentage, IGENITY™ L, *Tender*GENE tenderness, *Double*BLACK coat color

- http://www.immgen.com
  Parentage, Complex Vertebral Malformation (CVM)*,* BLAD, DUMPS, Kappa-Casein, Beta-lactoglobulin, Pompe's disease

Reference

Taylor, R. E. and T. G. Field. 2002. Beef Production and Management Decisions. 4th Edition. Prentice Hall, NJ.

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